

From: Clif McKee [clifton.mckee@gmail.com]
Sent: Wednesday, April 1, 2020 10:52 AM
To: Plowright, Raina [raina.plowright@montana.edu]
CC: Manuel Ruiz [m.ruiz.aravena@gmail.com]; Emily Gurley [egurley1@jhu.edu]
Subject: Re: call tmrw for MSU proposal to pivot to COVID-19 work
Attachments: Cui J et al [2019] Nature Rev Microbiol.pdf; Wong et al. - 2019 - Global epidemiology of bat coronaviruses.pdf; Banerjee et al. - 2019 - Bats and coronaviruses.pdf

I would be happy to co-lead with Manuel. Attached are the reviews that I've seen. They mostly cover viral diversity, evolution, and intermediate hosts - nothing much about shedding. I think we definitely have room to highlight the knowledge gaps in virus shedding from bats.

Manuel, would you be willing to share what you have put together already? A Zoom call would also be helpful to get on the same page and divide up the writing.

On Wed, Apr 1, 2020 at 12:39 PM Plowright, Raina <raina.plowright@montana.edu> wrote:

PS agree – highlight our groups potential to lead! I see this as the USAID draft.

From: Clif McKee <clifton.mckee@gmail.com>
Date: Wednesday, April 1, 2020 at 10:30 AM
To: Raina Plowright <raina.plowright@montana.edu>
Cc: Manuel Ruiz <m.ruiz.aravena@gmail.com>, Emily Gurley <egurley1@jhu.edu>
Subject: Re: call tmrw for MSU proposal to pivot to COVID-19 work

Hi Raina,

I think it is a fine idea, but I think we should work together on an outline. There are already some good reviews about CoVs in bats and it seems like everyone and their brother is writing some sort of commentary on COVID-19, so we ought to be strategic about what we want to say and how it will be a unique contribution that highlights our group's potential to lead in this field.

Best,

Clif

On Mon, Mar 30, 2020 at 3:47 PM Plowright, Raina <raina.plowright@montana.edu> wrote:

PS what are your thoughts on writing a quick review of what is known about CoVs in bats? Given you have just done this great job with literature, I think you could get something together quickly... could probably propose somewhere like nature communications, bring on collaborators from other parts of our project. I think other groups may already be doing this, so speed would be of essence.

Cc'ing Emily as I know Clif has other priorities too... and Manuel you are sitting on another draft and the COVID response is taking time... I'm thinking beyond COVID and how to place ourselves as the experts in the area of ecology of pathogen shedding... let me know your thoughts... I'd be excited by this. Could help you outline something.

From: Clif McKee <clifton.mckee@gmail.com>
Date: Monday, March 30, 2020 at 11:56 AM
To: Raina Plowright <raina.plowright@montana.edu>
Cc: Manuel Ruiz <m.ruiz.aravena@gmail.com>
Subject: Re: call tmrw for MSU proposal to pivot to COVID-19 work

Found some more:

lineage D in *P. medius* guano from Sri Lanka
<https://doi.org/10.1111/tbed.12851>

Australian *P. alecto* (Smith et al. 2016) <https://doi.org/10.1007/s10393-016-1116-x>

On Mon, Mar 30, 2020 at 1:53 PM Plowright, Raina
<raina.plowright@montana.edu> wrote:

THANK YOU!!!

From: Clif McKee <clifton.mckee@gmail.com>
Date: Monday, March 30, 2020 at 11:52 AM
To: Raina Plowright <raina.plowright@montana.edu>
Cc: Manuel Ruiz <m.ruiz.aravena@gmail.com>
Subject: Re: call tmrw for MSU proposal to pivot to COVID-19 work

It's lineage D, the one that contains HKU9 and is mainly in pteropodids. Mendenhall 2017 Transboundary and Emerging Disease did a nice review of that lineage.

On Mon, Mar 30, 2020 at 1:50 PM Plowright, Raina <raina.plowright@montana.edu> wrote:

Medius and Alecto have betacoronaviruses but I can't remember which lineage and can't find the right paper – its not lineage B right? (with SARS)

From: Manuel Ruiz <m.ruiz.aravena@gmail.com>
Date: Monday, March 30, 2020 at 8:37 AM
To: Clif McKee <clifton.mckee@gmail.com>
Cc: Alison Peel <a.peel@griffith.edu.au>, Raina Plowright <raina.plowright@montana.edu>, Emily Gurley <egurley1@jhu.edu>
Subject: Re: call tmrw for MSU proposal to pivot to COVID-19 work

Hi Clif,

I started a google doc so we could work together/coordinated.

this is the link

https://docs.google.com/document/d/1O_MoXNaaCfLwOyVH6D-WBYVoQcUKB2ZGITSEt7cj25c/edit?usp=sharing

Cheers,

Manuel

Manuel Ruiz Aravena

Postdoctoral Researcher

Department of Microbiology and Immunology
| Montana State University, USA

Mobile: +1 (406) 588 - 2551

El lun., 30 mar. 2020 a las 7:34, Clif McKee
(<clifton.mckee@gmail.com>) escribió:

Hi Raina,

I'll prioritize getting this done this morning.

Best,

Clif

On Sun, Mar 29, 2020 at 11:40 PM Alison Peel
<a.peel@griffith.edu.au> wrote:

Some quick thoughts from me before I have to put the
computer down for the day.

A reminder, that these two fact sheets provide useful
reference:

- https://www.wildlifehealthaustralia.com.au/Portals/0/Documents/FactSheets/Public%20health/Novel_coronavirus-2019.pdf

- https://www.wildlifehealthaustralia.com.au/Portals/0/Documents/FactSheets/Mammals/Coronaviruses_in_Australian_Bats.pdf

2. What is the relevance of the collection sites (Bangladesh, Australia) regarding to CoV spillover:

a. What is the prevalence of CoV in these areas of the world and the frequency of spillover there (and to what species)? Do we have seroprevalence data for humans exposed to CoV in these areas?

Prevalence in bats (presumably he's referring to bats?) - Craig Smith's paper and Peter Holz's recent thesis (?+paper) will have exact figures on prevalence, *but* surveillance has been extremely patchy and these figures are not likely to be fully representative. But Kevin Ollival's paper (Young, C. C. W. and K. J. Ollival (2016). "Optimizing Viral Discovery in Bats." Plos One 11(2).) documents how widespread CoV are (maybe in supp info) across many/all bat species, so we would expect it to be the same here in oz. There just haven't been extensive studies.

I would hazard a guess that the frequency of spillover is unstudied.

I'm not sure about seroprevalence data in people.

b. If CoV is present in bat species in these areas of the world, why it has never spilled over into humans or caused any outbreaks?

Australia - different population structure and opportunities to interact closely with bats. Likely human spillover population would be bat carers, possibly cavers. I need to think more about this but out of time now.

c. Would it be useful to compare the dynamics of CoV in bats from these areas of the world (Bangladesh/Australia) vs China where the virus has spilled over more frequently?

Many CoV studies (incl temporal studies) have been in insectivorous/hibernating bats. It would be useful to compare

dynamics in hibernating vs non-hibernating bats to look for seasonal/aseasonal drivers.

I'll try to keep an eye on emails/slack later tonight when I'm back on my computer to see if we can throw some ideas around.

Cheers

Ali

On Mon, 30 Mar 2020 at 13:19, Plowright, Raina
<raina.plowright@montana.edu> wrote:

Hi Manuel and Clif,

Could you spare some time tomorrow morning to help provide comprehensive answers to the questions below?

2. What is the relevance of the collection sites (Bangladesh, Australia) regarding to CoV spillover:
 - a. What is the prevalence of CoV in these areas of the world and the frequency of spillover there (and to what species)? Do we have seroprevalence data for humans exposed to CoV in these areas?
 - b. If CoV is present in bat species in these areas of the world, why it has never spilled over into humans or caused any outbreaks?
 - c. Would it be useful to compare the dynamics of CoV in bats from these areas of the world (Bangladesh/Australia) vs China where the virus has spilled over more frequently?

This is urgent and I hope you can put it before all other things tomorrow. We are talking with Ro at 12PM MT.

Could you please look at the coronavirus literature and provide answers (and refer me to the relevant papers) to the questions. I won't have much time to work on this before the call so will very much rely on your help.

Ali, if you have any ideas tonight, please shoot them to me.

Thanks,

Raina

Begin forwarded message:

From: "Chitale, Rohit"
<rohit.chitale@darpa.mil>

Subject: RE: call tmrw for MSU
proposal to pivot to COVID-19 work

Date: March 29, 2020 at 6:02:21 PM
MDT

To: "Plowright, Raina"
<raina.plowright@montana.edu>,
"LaTrielle, Sara"

<sara.latrielle@montana.edu>,
"alex.d.washburne@gmail.com"
<alex.d.washburne@gmail.com>, Peter
Hudson <pjh18@psu.edu>

Cc: "Zamisch, Monica (contr-bto)"
<monica.zamisch.ctr@darpa.mil>,
"Kumar, Srikanta (contr-i2o)"
<Srikanta.Kumar.ctr@darpa.mil>,
"Skinner, Anna (contr-sto)"
<anna.skinner.ctr@darpa.mil>, "Rich,
Shawn (contr-bto)"
<shawn.rich.ctr@darpa.mil>

Dear Raina and team,

In anticipation of tmrw's call (DARPA team,
please join if you are able), we had some
questions/thoughts (at bottom), sending
along for your review and then our
discussion tmrw.

Given these goals from your proposal:

1. Develop the first spatiotemporal dataset of coronavirus shedding from bat populations with existing metadata on bat demography, immune status, nutrition status, physiological status and coinfection status.
2. Understand how periods of coronavirus shedding coincide with multiviral shedding pulses observed for other viral families
3. Understand ecological drivers of pathogen shedding.
4. Allow to narrow down drivers of coronavirus shedding and spillover to inform surveillance of bat viruses with zoonotic potential globally, and help to prevent future pandemic events

Given this approach from your proposal:

The work proposed will leverage ongoing

PREEMPT work including collected samples, new knowledge on viral dynamics and bat behavior, and an established infrastructure, to address and predict a potential nCoV emergence in the future.

... a few questions/thoughts for tomorrow's discussion include:

1. What are the deliverables / actionable outcomes? Timelines?
2. What is the relevance of the collection sites (Bangladesh, Australia) regarding to CoV spillover:
 - a. What is the prevalence of CoV in these areas of the world and the frequency of spillover there (and to what species)? Do we have seroprevalence data for humans exposed to CoV in these areas?
 - b. If CoV is present in bat species in these areas of the world, why it has never spilled over into humans or caused any outbreaks?
 - c. Would it be useful to compare the dynamics of CoV in bats from these areas of the world (Bangladesh/Australia) vs China where the virus has spilled over more frequently?
3. We would like you to consider a potential collaboration with EcoHealth Alliance (or another competent organization) that has samples from China in order to understand better what are key factors that drive spillover events esp wrt nCoV.

Best,
Ro